

RAW SEQUENCE LISTING

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Application Serial Number:

10/524,647

Source:

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2-26-05

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RAW SEQUENCE LISTING

DATE: 02/26/2005

PATENT APPLICATION: US/10/524,647

TIME: 10:52:55

Input Set : A:\Final sequence list-13173-00004-US.txt

Output Set: N:\CRF4\02262005\J524647.raw

3 <110> APPLICANT: Flachmann, Ralf
 4 Sauer, Matt
 5 Schopfer, Christel R.
 6 Klebsattel, Martin
 7 Pfeiffer, Angelika-Maria
 8 Luck, Thomas
 9 Voeste, Dirk

11 <120> TITLE OF INVENTION: Use of astaxanthin-containing plants or parts of plants of
 the
 12 genus Tagetes as feedstuffs

14 <130> FILE REFERENCE: 13173-00004-US

C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/524,647

C--> 16 <141> CURRENT FILING DATE: 2005-02-17

16 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/009109

17 <151> PRIOR FILING DATE: 2003-08-18

19 <150> PRIOR APPLICATION NUMBER: DE 102 38 980.2

20 <151> PRIOR FILING DATE: 2002-08-20

22 <150> PRIOR APPLICATION NUMBER: DE 102 38 978.0

23 <151> PRIOR FILING DATE: 2002-08-20

25 <150> PRIOR APPLICATION NUMBER: DE 102 38 979.9

26 <151> PRIOR FILING DATE: 2002-08-20

28 <150> PRIOR APPLICATION NUMBER: DE 102 53 112.9

29 <151> PRIOR FILING DATE: 2002-11-13

31 <150> PRIOR APPLICATION NUMBER: DE 102 58 971.2

32 <151> PRIOR FILING DATE: 2002-12-16

34 <160> NUMBER OF SEQ ID NOS: 142

36 <170> SOFTWARE: PatentIn version 3.3

39 <210> SEQ ID NO: 1

41 <211> LENGTH: 1771

43 <212> TYPE: DNA

45 <213> ORGANISM: Haematococcus pluvialis

47 <220> FEATURE:

49 <221> NAME/KEY: CDS

51 <222> LOCATION: (166)..(1155)

53 <400> SEQUENCE: 1

54	ggcagcagct tgcacgcaag tcagcgcgcg caagtcaaca cctgccggtc cacagcctca	60
56	aataataaag agctcaagcg tttgtgcgcc tcgacgtggc cagtctgcac tgccttgaac	120
58	ccgcgagtct cccgcgcgcac tgactgccat agcacagcta gacga atg cag cta gca	177
59	Met Gln Leu Ala	
60	1	
62	gcg aca gta atg ttg gag cag ctt acc gga agc gct gag gca ctc aag	225
63	Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys	
64	5 10 15 20	
66	gag aag gag aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg	273

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67 Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp
68                25                30                35
70 gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg      321
71 Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro
72                40                45                50
74 gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc      369
75 Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile
76                55                60                65
78 aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac      417
79 Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His
80                70                75                80
82 gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg      465
83 Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp
84 85                90                95                100
86 ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc      513
87 Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser
88                105                110                115
90 ctg ctc gac atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca      561
91 Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr
92                120                125                130
94 ggc ctt ttt atc acc acg cat gat gct atg cat ggc acc atc gcc atg      609
95 Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met
96                135                140                145
98 aga aac agg cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg      657
99 Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu
100                150                155                160
102 tac gcc tgg ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac      705
103 Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His
104 165                170                175                180
106 cac aac cac act ggc gag gtg ggc aag gac cct gac ttc cac agg gga      753
107 His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly
108                185                190                195
110 aac cct ggc att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg      801
111 Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met
112                200                205                210
114 tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag      849
115 Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln
116                215                220                225
118 ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg      897
119 Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala
120                230                235                240
122 ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc      945
123 Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro
124 245                250                255                260
126 cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg      993
127 His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met
128                265                270                275
130 aac tgg tgg aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt      1041
131 Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe

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132          280          285          290
134 ctg acc tgc tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc      1089
135 Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro
136          295          300          305
138 ttc gcc ccc tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga      1137
139 Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg
140          310          315          320
142 ggt ctg gtt cct gcc tag ctggacacac tgcagtgggc cctgctgcca      1185
143 Gly Leu Val Pro Ala
144 325
146 gctgggcatg caggttgtgg caggactggg tgaggtgaaa agctgcaggc gctgctgccg      1245
148 gacacgctgc atgggctacc ctgtgtagct gccgccacta ggggaggggg tttgtagctg      1305
150 tcgagcttgc cccatggatg aagctgtgta gtggtgcagg gagtacaccc acaggccaac      1365
152 acccttgacg gagatgtctt gcgtcgggag gagtggtggg cagtgtagat gctatgattg      1425
154 tatcttaatg ctgaagcctt taggggagcg acacttagtg ctgggcaggc aacgccttgc      1485
156 aagggtgcagg cacaagctag gctggacgag gactcggtag caggcagggtg aagaggtgcg      1545
158 ggagggtggt gccacaccca ctgggcaaga ccatgctgca atgctggcgg tgtggcagtg      1605
160 agagctgcgt gattaactgg gctatggatt gtttgagcag tctcacttat tctttgatat      1665
162 agatactggt caggcagggtc aggagagtga gtatgaacaa gttgagaggt ggtgcgctgc      1725
164 ccctgcgctt atgaagctgt aacaataaag tggttcaaaa aaaaaa      1771
167 <210> SEQ ID NO: 2
169 <211> LENGTH: 329
171 <212> TYPE: PRT
173 <213> ORGANISM: Haematococcus pluvialis
175 <400> SEQUENCE: 2
177 Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
178 1          5          10          15
181 Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
182          20          25          30
185 Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
186          35          40          45
189 Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
190          50          55          60
193 Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
194 65          70          75          80
197 Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
198          85          90          95
201 Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
202          100          105          110
205 Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu
206          115          120          125
209 Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
210          130          135          140
213 Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
214 145          150          155          160
217 Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
218          165          170          175
221 His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
222          180          185          190

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225 Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
226      195      200      205
229 Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
230      210      215      220
233 Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
234 225      230      235      240
237 Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
238      245      250      255
241 Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
242      260      265      270
245 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
246      275      280      285
249 Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
250      290      295      300
253 His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
254 305      310      315      320
257 Leu Ser Gly Arg Gly Leu Val Pro Ala
258      325
261 <210> SEQ ID NO: 3
263 <211> LENGTH: 1662
265 <212> TYPE: DNA
267 <213> ORGANISM: Haematococcus pluvialis
269 <220> FEATURE:
271 <221> NAME/KEY: CDS
273 <222> LOCATION: (168)..(1130)
275 <400> SEQUENCE: 3
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278 gctatcgacg tggttgtgag cgctcgacgt ggtccactga cgggcctgtg agcctctgcg      120
280 ctccgtcctc tgccaaatct cgcgtcgggg cctgcctaag tcgaaga atg cac gtc      176
281      Met His Val
282      1
284 gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc      224
285 Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser
286      5      10      15
288 agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc      272
289 Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser
290 20      25      30      35
292 gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct      320
293 Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro
294      40      45      50
296 cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc      368
297 Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly
298      55      60      65
300 acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg      416
301 Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro
302      70      75      80
304 aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc      464
305 Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala
306      85      90      95

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308 cag ctt ttg ggc gga agc agc agc cta ctg cac atc gct gca gtc ttc      512
309 Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe
310 100      105      110      115
312 att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac      560
313 Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp
314      120      125      130
316 gca atg cat ggc acc ata gct ttg agg cac agg cag ctc aat gat ctc      608
317 Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu
318      135      140      145
320 ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac tac agc atg      656
321 Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met
322      150      155      160
324 ctg cat cgc aag cac tgg gag cac cac aac cat act ggc gaa gtg ggg      704
325 Leu His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly
326      165      170      175
328 aaa gac cct gac ttc cac aag gga aat ccc ggc ctt gtc ccc tgg ttc      752
329 Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe
330 180      185      190      195
332 gcc agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg      800
333 Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu
334      200      205      210
336 gca tgg tgg gca gtg gtg atg caa atg ctg ggg gcg ccc atg gca aat      848
337 Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn
338      215      220      225
340 ctc cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc      896
341 Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu
342      230      235      240
344 ttc tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca      944
345 Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala
346      245      250      255
348 gca ggc tct cag gtg atg gcc tgg ttc agg gcc aag aca agt gag gca      992
349 Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala
350 260      265      270      275
352 tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg      1040
353 Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp
354      280      285      290
356 gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc      1088
357 Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys
358      295      300      305
360 cgc cgc ctg tcc ggg cgt ggc ctg gtg cct gcc ttg gca tga      1130
361 Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala
362      310      315      320
364 cctggctcct ccgctggtga cccagcgtct gcacaagagt gtcattgctac aggggtgctgc      1190
366 ggccagtggc agcgcagtgc actctcagcc tgtatggggc taccgctgtg ccactgagca      1250
368 ctgggcatgc cactgagcac tgggcgtgct actgagcaat gggcgtgcta ctgagcaatg      1310
370 ggcgtgctac tgacaatggg cgtgctactg gggctctggca gtggctagga tggagtttga      1370
372 tgcattcagt agcgggtggc aacgtcatgt ggatgggtgga agtgctgagg ggtttaggca      1430
374 gccggcattt gagagggcta agttataaat cgcattgctgc tcatgcgcac atatctgcac      1490
376 acagccaggg aaatcccttc gagagtgatt atgggacact tgtattgggt tcgtgctatt      1550

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VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Current Application No

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:3445 M:283 W: Missing Blank Line separator, <220> field identifier